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Multivariate analysis of wild germplasm of rice

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Abstract

In plant breeding, characterization of different morphological traits is the basis requirement for selection of the breeding programme. In present study, forty wild germplasms received from National Research Center on Plant Biotechnology, New Delhi were included to characterize them on the bases of twelve morphological traits. This study was conducted at rice experimental field of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India during *kharif* season, 2018. To study the variation and to determine the relative contribution of various traits for total variability, Principal component analysis was used. The first four principal component exhibited more than one Eigen value like PC 1 with value 4.5003 and PC 2 with 2.5923 PC 3 with 1.5991 and PC 4 with 1.2348 and these four principal components accounted for 82.72 percent of the total variation. The genotypes WRG(NKS)-440 along PCA I axis and WRG(NKS)-401 along PCA II axis identified on extreme positive side on both the axis were considered to be the best genotypes. These genotypes can be best for future breeding program in rice. The characters *viz*., days of flowering, panicle length and spike fertility explained the maximum variance in PC 1. These results of principal component analysis shows the high genetic variation and hence this population group and characters can be suitable for further breeding programme for rice improvement.

Keywords: Wild germplasm, rice, principal component analysis, breeding and Eigen value

Introduction

Rice is a monocotyledonous crop scientifically known as *Oryza sativa* L. It is an angiosperm crop belongs to the family of Poaceae and sub family Oryzoideae. *Indica*, *Japonica* and *Javanica* are the three sub species of rice. *Oryza sativa and Oryza glaberrima* are two species out of twenty-four species which are suitable for cultivation in genus Oryza and remaining species are wild type. *Oryza sativa* also known as Asian rice are grown globally while African rice *Oryza glaberrima* grown in West Africa. At global level 2.7 billion peoples are consume rice as staple food (Tenorioet *et al*., 2013) [9]. In India it provides 43% of caloric requirement for large portion of Indian population which is around 70% of population and that's why rice is consider as staple food of India. Due to increasing population of India the food requirement also increasing day by day and to fulfill food requirement high yielding varieties are required. To develop a high yielding variety a breeding program is completely depends upon the diversity present in germplasm. Multivariate analysis based on different methods like Principal Component Analysis (PCA), Cluster analysis and Discriminate analysis are useful to identify and summarize the heritable variation present in germplasm (Oyelola, 2004) [7]. In breeding program among different methods of multivariate analysis, principle component analysis (PCA) is very effective method for selection of genotypes based on diversity (Mohammadi and Prasanna, 2003) [4]. Pricipal Component Analysis (PCA) has been used in many divergence studies in rice (Maji and Shaibu, 2012; Gana *et al*., 2013; Nachimuthu *et al*., 2014) [3, 2, 6]. The present study was conducted to select genotypes based on genetic variance for rice improvement program. The current study was planned to select out the traits that sort the genotypes into different groups and suggest potential genotypes that could be used as parents in the rice improvement program

Materials and Methods

Forty late maturing wild rice germplasm lines (*Oryza nivara* and *Oryza rufipogon*) (Table1) received from Dr. N. K. Singh, National Research Center on Plant Biotechnology, New Delhi were used in this study. The genotypes were cultivated in RBD design with three replications at rice experiment farm of Institute of Agricultural Sciences, Banaras Hindu University, Varanasi, Uttar Pradesh, India during *kharif* season, 2018.

The morphological traits used in present study *viz.* days of fifty percent flowering (DF), days of maturity (DM), unfilled grain per panicle (UF), filled grain per panicle (FG), effective tillers per plant (ET), total grain per panicle (TGT), panicle weight (PWT; g), plant height (PHT; cm), Panicle Length (cm), test weight (T Wt.; gm), spikelet fertility (SF) and grain yield per plant (GPP; gm). Five randomly selected plants from each genotype were used for observation. For PCA analysis Statistical Tool for Agricultural Research (STAR) software was used.

Table 1: List of forty wild germplasm of rice

S. No.	Name of germplasm	S. No.	Name of germplasm
1	WRG(NKS)-401	11	WRG(NKS)-411
2	WRG(NKS)-402	12	WRG(NKS)-412
3	WRG(NKS)-403	13	WRG(NKS)-413
4	WRG(NKS)-404	14	WRG(NKS)-414
5	WRG(NKS)-405	15	WRG(NKS)-415
6	WRG(NKS)-406	16	WRG(NKS)-416
7	WRG(NKS)-407	17	WRG(NKS)-417
8	WRG(NKS)-408	18	WRG(NKS)-418
9	WRG(NKS)-409	19	WRG(NKS)-419
10	WRG(NKS)-410	20	WRG(NKS)-420

Results and Discussion

Forty germplasm of rice were grouped on the bases of Principal Component Scores (PCs). First four principal components with more than one Eigen value contain major part of variation which is about 82.72 percent of total variation and same type of finding was reported by Syafii *et al.* (2015) [8] and Dudhe *et al.* (2018) [1] (Table 2). Remaining principal components those have less than one Eigen value considered as non-significant in this study (Mustafa *et al.*, 2015) [5]. The major portion of variability was contributed by the PC1 (37.50%) among the all set of PCs and second largest contributor of variation was PC2 accounted for 21.60% of total variability. The factor loadings of different variables that were obtained by using PCA are presented in Table 2. In PC1 all characters showed positive factor loadings. In PC2 days of 50 percent flowering, panicle weight, plant height, test weight and spikelet fertility decoded negative loading while remaining characters with positive loading. In PC 3 only five traits with positive loading *viz.* panicle weight, plant height, panicle length and grain per panicle while remaining with negative loading. In PC4 only four traits with positive loading like days of maturity, panicle weight, plant height and test weight decoded positive loading while remaining with negative loading (Table 3). The PCA scores for forty rice genotypes in the first three PCs were analyzed and considered three axes as X, Y and Z; and squared distance of each genotype from these three axes were computed (Table 4). The distribution of all the lines under study is presented in Figure 1. The genotypes identified on extreme positive side on both the axis were considered to be the best genotypes *i.e.* genotypes (40) WRG (NKS)-440(5.42), (21) WRG (NKS) - 421(4.70), WRG (NKS) - 420(4.57) and (34) WRG (NKS) - 434 (4.17) along PCA I axis and genotypes (1) WRG (NKS) - 401 (3.59), (6) WRG (NKS) - 406 (3.56), (8) WRG (NKS) - 408 (2.32) and (40) WRG (NKS) - 440 (2.13) along PCA II axis.

These genotypes seven genotypes *viz.*, WRG (NKS)-440, WRG (NKS)-421, WRG (NKS)-420, WRG (NKS)-434, WRG (NKS)-401, WRG (NKS)-406 and WRG (NKS)-408 with maximum divergence can be useful for future breeding program in rice. The prominent traits like panicle weight, test weight, spikelet fertility and total grain yield coming together in different principal components and contributing towards explaining the variability. These traits and genotypes may be kept into consideration during breeding program.

Table 2: Eigen values and percent variation accounted for the 12 PCs

Statistics	Eigen Values	Proportion of Variance	Cumulative Proportion
PC 1	4.5003	0.3750	0.3750
PC 2	2.5923	0.2160	0.5910
PC 3	1.5991	0.1333	0.7243
PC 4	1.2348	0.1029	0.8272
PC 5	0.9733	0.0811	0.9083
PC 6	0.4171	0.0348	0.9431
PC 7	0.3339	0.0278	0.9709
PC 8	0.1468	0.0122	0.9831
PC 9	0.1006	0.0084	0.9915
PC 10	0.0597	0.0050	0.9965
PC 11	0.0422	0.0035	1.0000
PC 12	0.0000	0.0000	1.0000

Table 3: Factor loading of twelve traits with respect to the significant PCs

Variables	PC1	PC 2	PC 3	PC 4
DF	0.0686	-0.5300	-0.0738	-0.3708
DM	0.1377	0.0857	-0.7066	0.1513
UF	0.4390	0.1283	-0.0531	-0.1677
FG	0.4255	0.1359	-0.2273	-0.1106
ET	0.3722	0.1652	-0.0024	-0.1824
TGT	0.4278	0.1461	-0.0538	-0.0668
PWT	0.2568	-0.4149	0.0279	0.3304
PHT	0.2612	-0.0641	0.3573	0.4403
Penicle L.	0.0503	0.0760	0.1719	-0.3628
T. Wt	0.2697	-0.3833	0.0001	0.3661
SF	0.0444	-0.5325	-0.0431	-0.4117
GPP	0.2637	0.1250	0.5272	-0.1526

Table 4: PCA scores of forty genotypes of rice

S. No.	Genotype	PC1 (X Vector)	PC2 (Y Vector)	PC3 (Z Vector)
1	WRG(NKS)-401	-1.82522	3.594941	-0.7884
2	WRG(NKS)-402	2.171784	-1.17028	-1.13023
3	WRG(NKS)-403	0.248399	-1.56423	-1.17925
4	WRG(NKS)-404	-1.38718	-1.80649	-1.68235
5	WRG(NKS)-405	-0.54111	-1.48466	1.158265
6	WRG(NKS)-406	-1.90792	3.565103	-1.3691
7	WRG(NKS)-407	-0.0638	-0.81042	-0.67171
8	WRG(NKS)-408	-2.91804	2.321376	0.519141
9	WRG(NKS)-409	-0.67799	-0.11354	0.078817
10	WRG(NKS)-410	-2.59002	-1.31083	0.303126

11	WRG(NKS)-411	-0.88185	0.96866	1.888612
12	WRG(NKS)-412	-1.06567	-0.55868	0.538472
13	WRG(NKS)-413	-1.15526	0.244662	2.430325
14	WRG(NKS)-414	-2.67292	1.860558	-0.27504
15	WRG(NKS)-415	-1.05037	-1.70187	-0.69004
16	WRG(NKS)-416	0.985747	-0.90861	0.754956
17	WRG(NKS)-417	-0.68915	-2.09937	1.769965
18	WRG(NKS)-418	1.082981	-1.23655	0.97494
19	WRG(NKS)-419	0.788604	-1.2865	0.06753
20	WRG(NKS)-420	4.575875	0.455518	-0.528
21	WRG(NKS)-421	4.708338	-0.53209	1.090945
22	WRG(NKS)-422	0.76189	-1.75914	1.708977
23	WRG(NKS)-423	-1.32362	-1.36492	1.020647
24	WRG(NKS)-424	-1.0714	1.658792	-1.21985
25	WRG(NKS)-425	-2.30925	2.046621	-0.28798
26	WRG(NKS)-426	-2.89563	-3.94971	-2.69947
27	WRG(NKS)-427	-2.05536	0.951019	0.537985
28	WRG(NKS)-428	0.139287	-0.71288	1.168244
29	WRG(NKS)-429	2.758682	0.988061	-2.28678
30	WRG(NKS)-430	0.344346	-1.2394	-1.78806
31	WRG(NKS)-431	-1.9083	-0.22079	0.881648
32	WRG(NKS)-432	-0.9797	1.387234	-0.17172
33	WRG(NKS)-433	-0.47039	0.662596	-0.19962
34	WRG(NKS)-434	4.175168	1.316147	-0.60162
35	WRG(NKS)-435	-0.31139	0.789605	1.507696
36	WRG(NKS)-436	1.204767	1.00642	1.817282
37	WRG(NKS)-437	1.22509	0.140783	0.028146
38	WRG(NKS)-438	2.01743	-0.20997	-0.47004
39	WRG(NKS)-439	0.136193	-0.05208	-2.4119
40	WRG(NKS)-440	5.426943	2.134894	0.205462

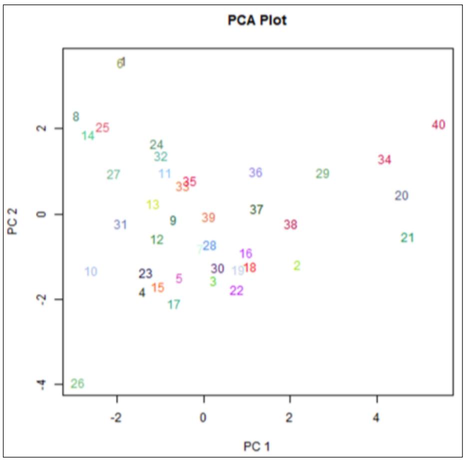

Fig 1: Distribution of breeding lines across two components

Conclusions

The present study was conducted to investigate the level of genetic divergence present in forty wild genotypes. Under principal component analysis out of forty genotypes, seven genotypes were identified *viz.*, WRG (NKS)-440, WRG (NKS)-421, WRG (NKS)-420, WRG (NKS)-434, WRG (NKS)-401, WRG (NKS)-406 and WRG (NKS)-408 with maximum divergence with better performance for panicle weight, test weight, spikelet fertility and total grain yield. So, for future breeding program in rice these genotypes can be used for enhancing rice yield.

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